REMARKS

Claim Status

Applicant has added claim 72; amended claims 1, 4, 5, 12-14, 18, 19, 24, 26, 29, 43-49, 57, 62, and 64; and cancelled claims 2, 7, 9-11, 25, 27, 28, 30-42, 50-56, 58-61, 63, and 65-71. Claims 3, 6, 8, and 15-17 were cancelled by earlier amendments. Accordingly, claims 1, 4, 5, 12-14, 18-24, 26, 29, 43-49, 57, 62, 64, and 72 are pending. Applicant acknowledges, with thanks, the Examiner's allowance of claims 1, 4, 5, 7, 9-14, 18-23, 29, 43, 46-49, 57, and 60-69 in the Office Action mailed April 30, 2008.

Claims 1, 24, 26, 29, and 57 have been amended to more distinctly claim subject matter. Claims 1, 4, 5, 12-14, 26, 62, and 64 have been amended to recite "SEQ ID NO:" instead of "SEQ ID No" Claims 4, 5, 12, 18, 19, 29, 43, 46-49, 57, 62 and 64 have been amended to depend from new claim 72. Claims 4, 5, 14, 62, and 64 have also been amended to further vary in scope from claim 72. Claims 44 and 45 have been amended to depend from previously allowed claim 43. In Applicant's Amendment and Response filed February 4, 2008, claims 44 and 45 were recited as withdrawn since, as-filed, these claims incorrectly depended from withdrawn claim 40—drawn to non-elected restriction Group II, from the Restriction Requirement mailed April 25, 2007. Applicant respectfully requests the Examiner's consideration and allowance of these previously withdrawn claims, which read on the elected invention and depend from an allowed claim.

The claim amendments are fully supported by the application as-filed, for example, on page 6 lines 1-13; page 6 line 18- page 7, line 15; pages 53-55; page 61, lines 4-12; and original claims 1, 4-7, 14, 18-24, 43-49, and 57. In particular, page 61 of

the as-filed specification recites that secretion of the antigen genes *esxBA* (SEQ ID NOs: 17 and 18, encoding CFP-10 and ESAT-6, respectively) is predicted to require upstream genes Rv3868-Rv3871 (SEQ ID NOs:11-14) and downstream genes Rv3876 and Rv3877 (SEQ ID NOs: 19 and 20). Thus, new claim 72, which recites, *inter alia,* a strain comprising sequences corresponding to SEQ ID NOs: 17, 18, 11-14; and 19 and 20, is fully supported by the application as-filed. Accordingly, no new matter is added and entry of the Amendment is courteously solicited.

All claim amendments are made without prejudice and Applicant reserves the right to pursue cancelled subject matter in one or more continuing applications.

Examiner interview

Applicant wishes to thank the Examiner for his availability, courtesy, and helpful comments during a telephone interview on July 21, 2008. Proposed claim amendments were briefly discussed and Applicant's representative explained an unintentional error made in the Response filed February 4, 2008, during discussion of the Mahairas et al. reference. The error and the appropriate correction are further described and made of record *infra.* No final agreements were reached. Applicant thanks the Examiner for his indication that he would consider this Response.

Claim objection

Claim 2 has been cancelled, rendering the rejection moot.

Indefiniteness

Claims 24-26, 70, and 71 were rejected under 35 U.S.C. § 112, second paragraph, as allegedly indefinite. Claim 24 was alleged to be unclear as to how many cosmids were included in the claimed strain. Claim 24 has been amended to read on a strain comprising a single cosmid. Claim 26 was alleged to be unclear as to what "said cosmid corresponding to" referred to, i.e., an exact sequence or a variant. Claim 26 has been amended to recite that the strain comprises a nucleic acid having the sequence shown in SEQ ID NO:1. Claims 25, 70, and 71 have been cancelled, rendering their rejection moot.

Accordingly, withdrawal of the rejection and reconsideration of the claims are respectfully requested.

Anticipation and correction

Original claims 1-11, 15-17, 44, and 45 were rejected in the Office Action mailed October 3, 2007 under 35 U.S.C. § 102(b) as allegedly anticipated by Mahairas et al. *J. Bacteriol.* 178:1274-82 (1996). In response, on February 4, 2008, Applicant submitted amended claims and arguments averring that Mahairas et al. disclosed an approximately 9.5 kb sequence containing six genes that may be encompassed by the instant approximately 32 kb SEQ ID NO:1, but which did not disclose the entirety of SEQ ID NO:1. For example, Applicant submitted that Mahairas did not disclose a mycobacterium containing DNA comprising at least seven genes or fragments thereof selected from SEQ ID NOs:4-28, which are encompassed by SEQ ID NO:1.

While preparing the Response to the present Office Action, Applicant's representatives became aware that Mahairas et al. disclosed a larger, approximately 17.5 kb sequence, which still may be encompassed by SEQ ID NO:1 (see attached sequence alignment A) but includes more than six genes. Applicant's representatives apologize for this unintentional error, which was made in earnest, without deceptive intent, and was only realized during preparation of this Response. This error was brought to the Examiner's attention during the interview of July 21, 2008.

Nevertheless, as amended, the instant claims are not anticipated by Mahairas et al. Sequences that are contained in SEQ ID NO:1, but not disclosed in Mahairas et al., include, for example, instant SEQ ID NOs:4-12 and 28[1]. See, e.g., attached sequence alignments. The pending claims all recite mycobacterium containing DNA sequences not taught by Mahairas et al. For example, Claim 1 requires a sequence corresponding to the entirety of SEQ ID NO:1 and thus comprises, e.g., SEQ ID NOs:4-12 and 28, which are not taught by Mahairas et al. New claim 72, from which the remaining claims depend, either directly or indirectly, requires the bacterium to comprise, *inter alia*, sequences corresponding to SEQ ID NOs:11 and 12, which are not taught by Mahaias

[1] The larger sequence of Mahairas et al., deposited under Genbank accession number U34848, corresponds, approximately, to nucleotides 11131-28578 of instant SEQ ID NO:1 (see attached sequence alignment A). Instant SEQ ID NO:13 corresponds to nucleotides 9673-11196 of SEQ ID NO:1 (see attached sequence alignment B) and SEQ ID NO:27 corresponds to nucleotides 28174-30030 (see attached sequence alignment C), and thus, are only partially overlapping with the sequence disclosed in Mahairas et al. Accordingly, instant SEQ ID NOs: 4-12 and 28 lie entirely outside of the region reported in Mahairas et al. Applicants note that WO 03/085098 is the international publication of PCT/IB03/01789, of which the instant application is a national stage entry under 35 U.S.C. § 371.

et al. Thus, Mahairas et al. does not teach all the elements of the instant claims and does not anticipate them.

CONCLUSION

Applicant respectfully requests that this Amendment under 37 C.F.R. § 1.116 be entered by the Examiner, placing all pending claims in condition for allowance. Applicant submits that the proposed amendments of the claims do not raise new issues or necessitate the undertaking of any additional search of the art by the Examiner, since all of the elements and their relationships claimed were either earlier claimed or inherent in the claims as examined. Therefore, this Amendment should allow for immediate action by the Examiner.

Finally, Applicant submits that the entry of the amendment would place the application in better form for appeal, should the Examiner dispute the patentability of the pending claims.

In view of the foregoing remarks, Applicant submits that this claimed invention, as amended, is neither anticipated nor rendered obvious in view of the prior art references cited against this application. Applicant therefore requests the entry of this Amendment, the Examiner's reconsideration and reexamination of the application, and the timely allowance of the pending claims.The Examiner is encouraged to contact the undersigned if it is believed that it would facilitate prosecution.

Please grant any extensions of time required to enter this response and charge any additional required fees to Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P.

Dated: July 30, 2008

By: _____
Laurence A. Shumway, Ph.D.
Reg. No. 61,169
(617) 452-1689

Attachments:

- Sequence Alignment A
- Sequence Alignment B
- Sequence Alignment C

Blast 2 Sequences results

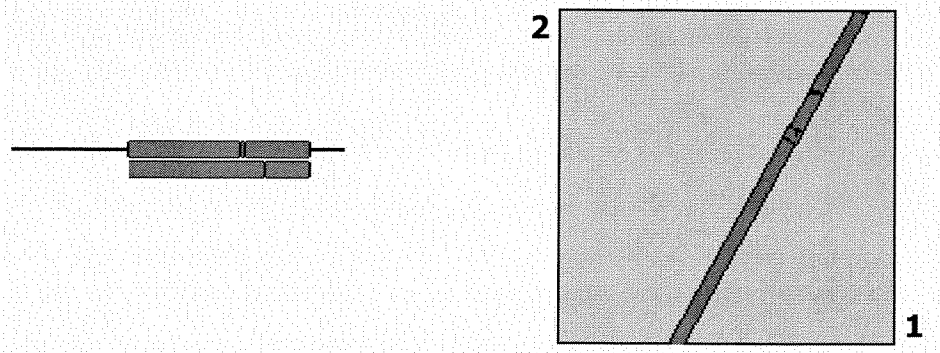
Alignment A

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 0 expect: 10.00 wordsize: 11 Filter ☐ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|40247167|emb|AX926815.1| Sequence 1 from Patent WO03085098
Length = 31808 (1 .. 31808)

Sequence 2: gi|1049222|gb|U34848.1| Mycobacterium bovis deletion region 1 Esat6 (esat6) gene, complete cds
Length = 17499 (1 .. 17499)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

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 Score = 3.322e+04 bits (17278),  Expect = 0.0
 Identities = 17436/17500 (99%), Gaps = 53/17500 (0%)
 Strand=Plus/Plus

Query  11131  GAATTCCTGCGCACCCTGATCCTGTCGCTGGTGGCAATGACTCATCCAGATCAGGTGAAT  11190
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Sbjct  1      GAATTCCTGCGCACCCTGATCCTGTCGCTGGTGGCAATGACTCATCCAGATCAGGTGAAT  60

Query  11191  CTCCTGCTCACCGACTTCAAAGGTGGTTCAACCTTCCTGGGAATGGAAAAGCTTCCGCAC  11250
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Sbjct  61     CTCCTGCTCACCGACTTCAAAGGTGGTTCAACCTTCCTGGGAATGGAAAAGCTTCCGCAC  120
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Query  11251  ACTGCCGCTGTCGTCACCAACATGGCCGAGGAAGCCGAGCTCGTCAGCCGGATGGGCGAG  11310
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Query  11311  GTGTTGACCGGAGAACTCGATCGGCGCCAGTCGATCCTCCGACAGGCCGGGATGAAAGTC  11370
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Sbjct  181    GTGTTGACCGGAGAACTCGATCGGCGCCAGTCGATCCTCCGACAGGCCGGGATGAAAGTC  240

Query  11371  GGCGCGGCCGGAGCCCTGTCCGGCGTGGCCGAATACGAGAAGTACCGCGAACGCGGTGCC  11430
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Query  11431  GACCTACCCCCGCTGCCAACGCTTTTCGTCGTCGTCGACGAGTTCGCCGAGCTGTTGCAG  11490
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Sbjct  2401     GGGTTGCACATCATTGTCACCTGTCAGATGAGCCAGGCTTACAAGGCAACCATGGACAAG  2460

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Sbjct  3061   CTATTCGCAAATCGACGACGGCGCCGCCGGCGTCTTCGCCTAATAGGCCCCCAACACATC  3120

Query  14251  GGAGGGAGTGATCACCATGCTGTGGCACGCAATGCCACCGGAGCTAAATACCGCACGGCT  14310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3121   GGAGGGAGTGATCACCATGCTGTGGCACGCAATGCCACCGGAGCTAAATACCGCACGGCT  3180

Query  14311  GATGGCCGGCGCGGGTCCGGCTCCAATGCTTGCGGCGGCCGCGGGATGGCAGACGCTTTC  14370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3181   GATGGCCGGCGCGGGTCCGGCTCCAATGCTTGCGGCGGCCGCGGGATGGCAGACGCTTTC  3240

Query  14371  GGCGGCTCTGGACGCTCAGGCCGTCGAGTTGACCGCGCGCCTGAACTCTCTGGGAGAAGC  14430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3241   GGCGGCTCTGGACGCTCAGGCCGTCGAGTTGACCGCGCGCCTGAACTCTCTGGGAGAAGC  3300

Query  14431  CTGGACTGGAGGTGGCAGCGACAAGGCGCTTGCGGCTGCAACGCCGATGGTGGTCTGGCT  14490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3301   CTGGACTGGAGGTGGCAGCGACAAGGCGCTTGCGGCTGCAACGCCGATGGTGGTCTGGCT  3360

Query  14491  ACAAACCGCGTCAACACAGGCCAAGACCCGTGCGATGCAGGCGACGGCGCAAGCCGCGGC  14550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3361   ACAAACCGCGTCAACACAGGCCAAGACCCGTGCGATGCAGGCGACGGCGCAAGCCGCGGC  3420

Query  14551  ATACACCCAGGCCATGGCCACGACGCCGTCGCTGCCGGAGATCGCCGCCAACCACATCAC  14610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3421   ATACACCCAGGCCATGGCCACGACGCCGTCGCTGCCGGAGATCGCCGCCAACCACATCAC  3480

Query  14611  CCAGGCCGTCCTTACGGCCACCAACTTCTTCGGTATCAACACGATCCCGATCGCGTTGAC  14670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3481   CCAGGCCGTCCTTACGGCCACCAACTTCTTCGGTATCAACACGATCCCGATCGCGTTGAC  3540

Query  14671  CGAGATGGATTATTTCATCCGTATGTGGAACCAGGCAGCCCTGGCAATGGAGGTCTACCA  14730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3541   CGAGATGGATTATTTCATCCGTATGTGGAACCAGGCAGCCCTGGCAATGGAGGTCTACCA  3600

Query  14731  GGCCGAGACCGCGGTTAACACGCTTTTCGAGAAGCTCGAGCCGATGGCGTCGATCCTTGA  14790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3601   GGCCGAGACCGCGGTTAACACGCTTTTCGAGAAGCTCGAGCCGATGGCGTCGATCCTTGA  3660

Query  14791  TCCCGGCGCGAGCCAGAGCACGACGAACCCGATCTTCGGAATGCCCTCCCCTGGCAGCTC  14850
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3661   TCCCGGCGCGAGCCAGAGCACGACGAACCCGATCTTCGGAATGCCCTCCCCTGGCAGCTC  3720

Query  14851  AACACCGGTTGGCCAGTTGCCGCCGGCGGCTACCCAGACCCTCGGCCAACTGGGTGAGAT  14910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3721   AACACCGGTTGGCCAGTTGCCGCCGGCGGCTACCCAGACCCTCGGCCAACTGGGTGAGAT  3780

Query  14911  GAGCGGCCCGATGCAGCAGCTGACCCAGCCGCTGCAGCAGGTGACGTCGTTGTTCAGCCA  14970
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3781   GAGCGGCCCGATGCAGCAGCTGACCCAGCCGCTGCAGCAGGTGACGTCGTTGTTCAGCCA  3840
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Query  14971  GGTGGGCGGCACCGGCGGCGGCAACCCAGCCGACGAGGAAGCCGCGCAGATGGGCCTGCT  15030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3841   GGTGGGCGGCACCGGCGGCGGCAACCCAGCCGACGAGGAAGCCGCGCAGATGGGCCTGCT  3900

Query  15031  CGGCACCAGTCCGCTGTCGAACCATCCGCTGGCTGGTGGATCAGGCCCCAGCGCGGGCGC  15090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3901   CGGCACCAGTCCGCTGTCGAACCATCCGCTGGCTGGTGGATCAGGCCCCAGCGCGGGCGC  3960

Query  15091  GGGCCTGCTGCGCGCGGAGTCGCTACCTGGCGCAGGTGGGTCGTTGACCCGCACGCCGCT  15150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3961   GGGCCTGCTGCGCGCGGAGTCGCTACCTGGCGCAGGTGGGTCGTTGACCCGCACGCCGCT  4020

Query  15151  GATGTCTCAGCTGATCGAAAAGCCGGTTGCCCCCTCGGTGATGCCGGCGGCTGCTGCCGG  15210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4021   GATGTCTCAGCTGATCGAAAAGCCGGTTGCCCCCTCGGTGATGCCGGCGGCTGCTGCCGG  4080

Query  15211  ATCGTCGGCGACGGGTGGCGCCGCTCCGGTGGGTGCGGGAGCGATGGGCCAGGGTGCGCA  15270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4081   ATCGTCGGCGACGGGTGGCGCCGCTCCGGTGGGTGCGGGAGCGATGGGCCAGGGTGCGCA  4140

Query  15271  ATCCGGCGGCTCCACCAGGCCGGGTCTGGTCGCGCCGGCACCGCTCGCGCAGGAGCGTGA  15330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4141   ATCCGGCGGCTCCACCAGGCCGGGTCTGGTCGCGCCGGCACCGCTCGCGCAGGAGCGTGA  4200

Query  15331  AGAAGACGACGAGGACGACTGGGACGAAGAGGACGACTGGTGAGCTCCCGTAATGACAAC  15390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4201   AGAAGACGACGAGGACGACTGGGACGAAGAGGACGACTGGTGAGCTCCCGTAATGACAAC  4260

Query  15391  AGACTTCCCGGCCACCCGGGCCGGAAGACTTGCCAACATTTTGGCGAGGAAGGTAAAGAG  15450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4261   AGACTTCCCGGCCACCCGGGCCGGAAGACTTGCCAACATTTTGGCGAGGAAGGTAAAGAG  4320

Query  15451  AGAAAGTAGTCCAGCATGGCAGAGATGAAGACCGATGCCGCTACCCTCGCGCAGGAGGCA  15510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4321   AGAAAGTAGTCCAGCATGGCAGAGATGAAGACCGATGCCGCTACCCTCGCGCAGGAGGCA  4380

Query  15511  GGTAATTTCGAGCGGATCTCCGGCGACCTGAAAACCCAGATCGACCAGGTGGAGTCGACG  15570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4381   GGTAATTTCGAGCGGATCTCCGGCGACCTGAAAACCCAGATCGACCAGGTGGAGTCGACG  4440

Query  15571  GCAGGTTCGTTGCAGGGCCAGTGGCGCGGCGCGGCGGGGACGGCCGCCCAGGCCGCGGTG  15630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4441   GCAGGTTCGTTGCAGGGCCAGTGGCGCGGCGCGGCGGGGACGGCCGCCCAGGCCGCGGTG  4500

Query  15631  GTGCGCTTCCAAGAAGCAGCCAATAAGCAGAAGCAGGAACTCGACGAGATCTCGACGAAT  15690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4501   GTGCGCTTCCAAGAAGCAGCCAATAAGCAGAAGCAGGAACTCGACGAGATCTCGACGAAT  4560

Query  15691  ATTCGTCAGGCCGGCGTCCAATACTCGAGGGCCGACGAGGAGCAGCAGCAGGCGCTGTCC  15750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  4561   ATTCGTCAGGCCGGCGTCCAATACTCGAGGGCCGACGAGGAGCAGCAGCAGGCGCTGTCC  4620

Query  15751  TCGCAAATGGGCTTCTGACCCGCTAATACGAAAAGAAACGGAGCAAAAACATGACAGAGC  15810
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4621   TCGCAAATGGGCTTCTGACCCGCTAATACGAAAAGAAACGGAGCAAAAACATGACAGAGC  4680

Query  15811  AGCAGTGGAATTTCGCGGGTATCGAGGCCGCGGCAAGCGCAATCCAGGGAAATGTCACGT  15870
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4681   AGCAGTGGAATTTCGCGGGTATCGAGGCCGCGGCAAGCGCAATCCAGGGAAATGTCACGT  4740

Query  15871  CCATTCATTCCCTCCTTGACGAGGGGAAGCAGTCCCTGACCAAGCTCGCAGCGGCCTGGG  15930
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4741   CCATTCATTCCCTCCTTGACGAGGGGAAGCAGTCCCTGACCAAGCTCGCAGCGGCCTGGG  4800

Query  15931  GCGGTAGCGGTTCGGAGGCGTACCAGGGTGTCCAGCAAAAATGGGACGCCACGGCTACCG  15990
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4801   GCGGTAGCGGTTCGGAGGCGTACCAGGGTGTCCAGCAAAAATGGGACGCCACGGCTACCG  4860

Query  15991  AGCTGAACAACGCGCTGCAGAACCTGGCGCGGACGATCAGCGAAGCCGGTCAGGCAATGG  16050
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4861   AGCTGAACAACGCGCTGCAGAACCTGGCGCGGACGATCAGCGAAGCCGGTCAGGCAATGG  4920

Query  16051  CTTCGACCGAAGGCAACGTCACTGGGATGTTCGCATAGGGCAACGCCGAGTTCGCGTAGA  16110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4921   CTTCGACCGAAGGCAACGTCACTGGGATGTTCGCATAGGGCAACGCCGAGTTCGCGTAGA  4980

Query  16111  ATAGCGAAACACGGGATCGGGCGAGTTCGACCTTCCGTCGGTCTCGCCCTTTCTCGTGTT  16170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4981   ATAGCGAAACACGGGATCGGGCGAGTTCGACCTTCCGTCGGTCTCGCCCTTTCTCGTGTT  5040

Query  16171  TATACGTTTGAGCGCACTCTGAGAGGTTGTCATGGCGGCCGACTACGACAAGCTCTTCCG  16230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5041   TATACGTTTGAGCGCACTCTGAGAGGTTGTCATGGCGGCCGACTACGACAAGCTCTTCCG  5100

Query  16231  GCCGCACGAAGGTATGGAAGCTCCGGACGATATGGCAGCGCAGCCGTTCTTCGACCCCAG  16290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5101   GCCGCACGAAGGTATGGAAGCTCCGGACGATATGGCAGCGCAGCCGTTCTTCGACCCCAG  5160

Query  16291  TGCTTCGTTTCCGCCGGCGCCCGCATCGGCAAACCTACCGAAGCCCAACGGCCAGACTCC  16350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5161   TGCTTCGTTTCCGCCGGCGCCCGCATCGGCAAACCTACCGAAGCCCAACGGCCAGACTCC  5220

Query  16351  GCCCCCGACGTCCGACGACCTGTCGGAGCGGTTCGTGTCGGCCCCGCCGCCGCCACCCCC  16410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5221   GCCCCCGACGTCCGACGACCTGTCGGAGCGGTTCGTGTCGGCCCCGCCGCCGCCACCCCC  5280

Query  16411  ACCCCCACCTCCGCCTCCGCCAACTCCGATGCCGATCGCCGCAGGAGAGCCGCCCTCGCC  16470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5281   ACCCCCACCTCCGCCTCCGCCAACTCCGATGCCGATCGCCGCAGGAGAGCCGCCCTCGCC  5340
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Query  16471  GGAACCGGCCGCATCTAAACCACCCACACCCCCCATGCCCATCGCCGGACCCGAACCGGC  16530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5341   GGAACCGGCCGCATCTAAACCACCCACACCCCCCATGCCCATCGCCGGACCCGAACCGGC  5400

Query  16531  CCCACCCAAACCACCCACACCCCCCATGCCCATCGCCGGACCCGAACCGGCCCCCACCCAA  16590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5401   CCCACCCAAACCACCCACACCCCCCATGCCCATCGCCGGACCCGAACCGGCCCCCACCCAA  5460

Query  16591  ACCACCCACACCTCCGATGCCCATCGCCGGACCTGCACCCACCCCAACCGAATCCCAGTT  16650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5461   ACCACCCACACCTCCGATGCCCATCGCCGGACCTGCACCCACCCCAACCGAATCCCAGTT  5520

Query  16651  GGCGCCCCCCAGACCACCGACACCACAAACGCCAACCGGAGCGCCGCAGCAACCGGAATC  16710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5521   GGCGCCCCCCAGACCACCGACACCACAAACGCCAACCGGAGCGCCGCAGCAACCGGAATC  5580

Query  16711  ACCGGCGCCCCACGTACCCTCGCACGGGCCACATCAACCCCGGCGCACCGCACCAGCACC  16770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5581   ACCGGCGCCCCACGTACCCTCGCACGGGCCACATCAACCCCGGCGCACCGCACCAGCACC  5640

Query  16771  GCCCTGGGCAAAGATGCCAATCGGCGAACCCCCGCCCGCTCCGTCCAGACCGTCTGCGTC  16830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5641   GCCCTGGGCAAAGATGCCAATCGGCGAACCCCCGCCCGCTCCGTCCAGACCGTCTGCGTC  5700

Query  16831  CCCGGCCGAACCACCGACCCGGCCTGCCCCCCAACACTCCCGACGTGCGCGCCGGGGTCA  16890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5701   CCCGGCCGAACCACCGACCCGGCCTGCCCCCCAACACTCCCGACGTGCGCGCCGGGGTCA  5760

Query  16891  CCGCTATCGCACAGACACCGAACGAAACGTCGGGAAGGTAGCAACTGGTCCATCCATCCA  16950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5761   CCGCTATCGCACAGACACCGAACGAAACGTCGGGAAGGTAGCAACTGGTCCATCCATCCA  5820

Query  16951  GGCGCGGCTGCGGGCAGAGGAAGCATCCGGCGCGCAGCTCGCCCCCGGAACGGAGCCCTC  17010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5821   GGCGCGGCTGCGGGCAGAGGAAGCATCCGGCGCGCAGCTCGCCCCCGGAACGGAGCCCTC  5880

Query  17011  GCCAGCGCCGTTGGGCCAACCGAGATCGTATCTGGCTCCGCCCACCCGCCCCGCGCCGAC  17070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5881   GCCAGCGCCGTTGGGCCAACCGAGATCGTATCTGGCTCCGCCCACCCGCCCCGCGCCGAC  5940

Query  17071  AGAACCTCCCCCCAGCCCCTCGCCGCAGCGCAACTCCGGTCGGCGTGCCGAGCGACGCGT  17130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5941   AGAACCTCCCCCCAGCCCCTCGCCGCAGCGCAACTCCGGTCGGCGTGCCGAGCGACGCGT  6000

Query  17131  CCACCCCGATTTAGCCGCCCAACATGCCGCGGCGCAACCTGATTCAATTACGGCCGCAAC  17190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6001   CCACCCCGATTTAGCCGCCCAACATGCCGCGGCGCAACCTGATTCAATTACGGCCGCAAC  6060

Query  17191  CACTGGCGGTCGTCGCCGCAAGCGTGCAGCGCCGGATCTCGACGCGACACAGAAATCCTT  17250
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6061   CACTGGCGGTCGTCGCCGCAAGCGTGCAGCGCCGGATCTCGACGCGACACAGAAATCCTT  6120

Query  17251  AAGGCCGGCGGCCAAGGGGCCGAAGGTGAAGAAGGTGAAGCCCCAGAAACCGAAGGCCAC  17310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6121   AAGGCCGGCGGCCAAGGGGCCGAAGGTGAAGAAGGTGAAGCCCCAGAAACCGAAGGCCAC  6180

Query  17311  GAAGCCGCCCAAAGTGGTGTCGCAGCGCGGCTGGCGACATTGGGTGCATGCGTTGACGCG  17370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6181   GAAGCCGCCCAAAGTGGTGTCGCAGCGCGGCTGGCGACATTGGGTGCATGCGTTGACGCG  6240

Query  17371  AATCAACCTGGGCCTGTCACCCGACGAGAAGTACGAGCTGGACCTGCACGCTCGAGTCCG  17430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6241   AATCAACCTGGGCCTGTCACCCGACGAGAAGTACGAGCTGGACCTGCACGCTCGAGTCCG  6300

Query  17431  CCGCAATCCCCGCGGGTCGTATCAGATCGCCGTCGTCGGTCTCAAAGGTGGGGCTGGCAA  17490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6301   CCGCAATCCCCGCGGGTCGTATCAGATCGCCGTCGTCGGTCTCAAAGGTGGGGCTGGCAA  6360

Query  17491  AACCACGCTGACAGCAGCGTTGGGGTCGACGTTGGCTCAGGTGCGGGCCGACCGGATCCT  17550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6361   AACCACGCTGACAGCAGCGTTGGGGTCGACGTTGGCTCAGGTGCGGGCCGACCGGATCCT  6420

Query  17551  GGCTCTAGACGCGGATCCAGGCGCCGGAAACCTCGCCGATCGGGTAGGGCGACAATCGGG  17610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6421   GGCTCTAGACGCGGATCCAGGCGCCGGAAACCTCGCCGATCGGGTAGGGCGACAATCGGG  6480

Query  17611  CGCGACCATCGCTGATGTGCTTGCAGAAAAAGAGCTGTCGCACTACAACGACATCCGCGC  17670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6481   CGCGACCATCGCTGATGTGCTTGCAGAAAAAGAGCTGTCGCACTACAACGACATCCGCGC  6540

Query  17671  ACACACTAGCGTCAATGCGGTCAATCTGGAAGTGCTGCCGGCACCGGAATACAGCTCGGC  17730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6541   ACACACTAGCGTCAATGCGGTCAATCTGGAAGTGCTGCCGGCACCGGAATACAGCTCGGC  6600

Query  17731  GCAGCGCGCGCTCAGCGACGCCGACTGGCATTTCATCGCCGATCCTGCGTCGAGGTTTTA  17790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6601   GCAGCGCGCGCTCAGCGACGCCGACTGGCATTTCATCGCCGATCCTGCGTCGAGGTTTTA  6660

Query  17791  CAACCTCGTCTTGGCTGATTGTGGGGCCGGCTTCTTCGACCCGCTGACCCGCGGCGTGCT  17850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6661   CAACCTCGTCTTGGCTGATTGTGGGGCCGGCTTCTTCGACCCGCTGACCCGCGGCGTGCT  6720

Query  17851  GTCCACGGTGTCCGGTGTCGTGGTCGTGGCAAGTGTCTCAATCGACGGCGCACAACAGGC  17910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6721   GTCCACGGTGTCCGGTGTCGTGGTCGTGGCAAGTGTCTCAATCGACGGCGCACAACAGGC  6780

Query  17911  GTCGGTCGCGTTGGACTGGTTGCGCAACAACGGTTACCAAGATTTGGCGAGCCGCGCATG  17970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6781   GTCGGTCGCGTTGGACTGGTTGCGCAACAACGGTTACCAAGATTTGGCGAGCCGCGCATG  6840
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Query  17971  CGTGGTCATCAATCACATCATGCCGGGAGAACCCAATGTCGCAGTTAAAGACCTGGTGCG  18030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6841   CGTGGTCATCAATCACATCATGCCGGGAGAACCCAATGTCGCAGTTAAAGACCTGGTGCG  6900

Query  18031  GCATTTCGAACAGCAAGTTCAACCCGGCCGGGTCGTGGTCATGCCGTGGGACAGGCACAT  18090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6901   GCATTTCGAACAGCAAGTTCAACCCGGCCGGGTCGTGGTCATGCCGTGGGACAGGCACAT  6960

Query  18091  TGCGGCCGGAACCGAGATTTCACTCGACTTGCTCGACCCTATCTACAAGCGCAAGGTCCT  18150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6961   TGCGGCCGGAACCGAGATTTCACTCGACTTGCTCGACCCTATCTACAAGCGCAAGGTCCT  7020

Query  18151  CGAATTGGCCGCAGCGCTATCCGACGATTTCGAGAGGGCTGGACGTCGTTGAGCGCACCT  18210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7021   CGAATTGGCCGCAGCGCTATCCGACGATTTCGAGAGGGCTGGACGTCGTTGAGCGCACCT  7080

Query  18211  GCTGTTGCTGCTGGTCCTACCGCCGCGGGGGCAACCGCTGCGCGGCCTGCCACCACCCGG  18270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7081   GCTGTTGCTGCTGGTCCTACCGCCGCGGGGGCAACCGCTGCGCGGCCTGCCACCACCCGG  7140

Query  18271  GTGACGATCCTGACCGGCAGACGGATGACCGATTTGGTACTGCCAGCGGCGGTGCCGATG  18330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7141   GTGACGATCCTGACCGGCAGACGGATGACCGATTTGGTACTGCCAGCGGCGGTGCCGATG  7200

Query  18331  GAAACTTATATTGACGACACCGTCGCGGTGCTTTCCGAGGTGTTGGAAGACACGCCGGCT  18390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7201   GAAACTTATATTGACGACACCGTCGCGGTGCTTTCCGAGGTGTTGGAAGACACGCCGGCT  7260

Query  18391  GATGTACTCGGCGGCTTCGACTTTACCGCGCAAGGCGTGTGGGCGTTCGCTCGTCCCGGA  18450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7261   GATGTACTCGGCGGCTTCGACTTTACCGCGCAAGGCGTGTGGGCGTTCGCTCGTCCCGGA  7320

Query  18451  TCGCCGCCGCTGAAGCTCGACCAGTCACTCGATGACGCCGGGGTGGTCGACGGGTCACTG  18510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7321   TCGCCGCCGCTGAAGCTCGACCAGTCACTCGATGACGCCGGGGTGGTCGACGGGTCACTG  7380

Query  18511  CTGACTCTGGTGTCAGTCAGTCGCACCGAGCGCTACCGACCGTTGGTCGAGGATGTCATC  18570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7381   CTGACTCTGGTGTCAGTCAGTCGCACCGAGCGCTACCGACCGTTGGTCGAGGATGTCATC  7440

Query  18571  GACGCGATCGCCGTGCTTGACGAGTCACCTGAGTTCGACCGCACGGCATTGAATCGCTTT  18630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7441   GACGCGATCGCCGTGCTTGACGAGTCACCTGAGTTCGACCGCACGGCATTGAATCGCTTT  7500

Query  18631  GTGGGGGCGGCGATCCCGCTTTTGACCGCGCCCGTCATCGGGATGGCGATGCGGGCGTGG  18690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7501   GTGGGGGCGGCGATCCCGCTTTTGACCGCGCCCGTCATCGGGATGGCGATGCGGGCGTGG  7560

Query  18691  TGGGAAACTGGGCGTAGCTTGTGGTGGCCGTTGGCGATTGGCATCCTGGGGATCGCTGTG  18750
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7561      TGGGAAACTGGGCGTAGCTTGTGGTGGCCGTTGGCGATTGGCATCCTGGGGATCGCTGTG  7620

Query  18751     CTGGTAGGCAGCTTCGTCGCGAACAGGTTCTACCAGAGCGGCCACCTGGCCGAGTGCCTA  18810
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7621      CTGGTAGGCAGCTTCGTCGCGAACAGGTTCTACCAGAGCGGCCACCTGGCCGAGTGCCTA  7680

Query  18811     CTGGTCACGACGTATCTGCTGATCGCAACCGCCGCAGCGCTGGCCGTGCCGTTGCCGCGC  18870
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7681      CTGGTCACGACGTATCTGCTGATCGCAACCGCCGCAGCGCTGGCCGTGCCGTTGCCGCGC  7740

Query  18871     GGGGTCAACTCGTTGGGGGCGCCACAAGTTGCCGGCGCCGCTACGGCCGTGCTGTTTTTG  18930
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7741      GGGGTCAACTCGTTGGGGGCGCCACAAGTTGCCGGCGCCGCTACGGCCGTGCTGTTTTTG  7800

Query  18931     ACCTTGATGACGCGGGGCGGCCCTCGGAAGCGTCATGAGTTGGCGTCGTTTGCCGTGATC  18990
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7801      ACCTTGATGACGCGGGGCGGCCCTCGGAAGCGTCATGAGTTGGCGTCGTTTGCCGTGATC  7860

Query  18991     ACCGCTATCGCGGTCATCGCGGCCGCCGCTGCCTTCGGCTATGGATACCAGGACTGGGTC  19050
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7861      ACCGCTATCGCGGTCATCGCGGCCGCCGCTGCCTTCGGCTATGGATACCAGGACTGGGTC  7920

Query  19051     CCCGCGGGGGGGATCGCATTCGGGCTGTTCATTGTGACGAATGCGGCCAAGCTGACCGTC  19110
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7921      CCCGCGGGGGGGATCGCATTCGGGCTGTTCATTGTGACGAATGCGGCCAAGCTGACCGTC  7980

Query  19111     GCGGTCGCGCGGATCGCGCTGCCGCCGATTCCGGTACCCGGCGAAACCGTGGACAACGAG  19170
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7981      GCGGTCGCGCGGATCGCGCTGCCGCCGATTCCGGTACCCGGCGAAACCGTGGACAACGAG  8040

Query  19171     GAGTTGCTCGATCCCGTCGCGACCCCGGAGGCTACCAGCGAAGAAACCCCGACCTGGCAG  19230
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8041      GAGTTGCTCGATCCCGTCGCGACCCCGGAGGCTACCAGCGAAGAAACCCCGACCTGGCAG  8100

Query  19231     GCCATCATCGCGTCGGTGCCCGCGTCCGCGGTCCGGCTCACCGAGCGCAGCAAACTGGCC  19290
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8101      GCCATCATCGCGTCGGTGCCCGCGTCCGCGGTCCGGCTCACCGAGCGCAGCAAACTGGCC  8160

Query  19291     AAGCAACTTCTGATCGGATACGTCACGTCGGGCACCCTGATTCTGGCTGCCGGTGCCATC  19350
                 ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8161      AAGCAACTTCTCATCGGATACGTCACGTCGGGCACCCTGATTCTGGCTGCCGGTGCCATC  8220

Query  19351     GCGGTCGTGGTGCGCGGGCACTTCTTTGTACACAGCCTGGTGGTCGCGGGTTTGATCACG  19410
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8221      GCGGTCGTGGTGCGCGGGCACTTCTTTGTACACAGCCTGGTGGTCGCGGGTTTGATCACG  8280

Query  19411     ACCGTCTGCGGATTTCGCTCGCGGCTTTACGCCGAGCGCTGGTGTGCGTGGGCGTTGCTG  19470
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8281      ACCGTCTGCGGATTTCGCTCGCGGCTTTACGCCGAGCGCTGGTGTGCGTGGGCGTTGCTG  8340
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Query  19471  GCGGCGACGGTCGCGATTCCGACGGGTCTGACGGCCAAACTCATCATCTGGTACCCGCAC  19530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8341   GCGGCGACGGTCGCGATTCCGACGGGTCTGACGGCCAAACTCATCATCTGGTACCCGCAC  8400

Query  19531  TATGCCTGGCTGTTGTTGAGCGTCTACCTCACGGTAGCCCTGGTTGCGCTCGTGGTGGTC  19590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8401   TATGCCTGGCTGTTGTTGAGCGTCTACCTCACGGTAGCCCTGGTTGCGCTCGTGGTGGTC  8460

Query  19591  GGGTCGATGGCTCACGTCCGGCGCGTTTCACCGGTCGTAAAACGAACTCTGGAATTGATC  19650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8461   GGGTCGATGGCTCACGTCCGGCGCGTTTCACCGGTCGTAAAACGAACTCTGGAATTGATC  8520

Query  19651  GACGGCGCCATGATCGCTGCCATCATTCCCATGCTGCTGTGGATCACCGGGGTGTACGAC  19710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8521   GACGGCGCCATGATCGCTGCCATCATTCCCATGCTGCTGTGGATCACCGGGGTGTACGAC  8580

Query  19711  ACGGTCCGCAATATCCGGTTCTGAGCCGGATCGGCTGATTGGCGGTTCCTGACAGAACAT  19770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8581   ACGGTCCGCAATATCCGGTTCTGAGCCGGATCGGCTGATTGGCGGTTCCTGACAGAACAT  8640

Query  19771  CGAGGACACGGCGCAGGTTTGCATACCTTCGGCGCCCGACAAATTGCTGCGATTGAGCGT  19830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8641   CGAGGACACGGCGCAGGTTTGCATACCTTCGGCGCCCGACAAATTGCTGCGATTGAGCGT  8700

Query  19831  GTGGCGCGTCCGGTAAAATTTGCTCGATGGGGAACACGTATAGGAGATCCGGCAATGGCT  19890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8701   GTGGCGCGTCCGGTAAAATTTGCTCGATGGGGAACACGTATAGGAGATCCGGCAATGGCT  8760

Query  19891  GAACCGTTGGCCGTCGATCCCACCGGCTTGAGCGCAGCGGCCGCGAAATTGGCCGGCCTC  19950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8761   GAACCGTTGGCCGTCGATCCCACCGGCTTGAGCGCAGCGGCCGCGAAATTGGCCGGCCTC  8820

Query  19951  GTTTTTCCGCAGCCTCCGGCGCCGATCGCGGTCAGCGGAACGGATTCGGTGGTAGCAGCA  20010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8821   GTTTTTCCGCAGCCTCCGGCGCCGATCGCGGTCAGCGGAACGGATTCGGTGGTAGCAGCA  8880

Query  20011  ATCAACGAGACCATGCCAAGCATCGAATCGCTGGTCAGTGACGGGCTGCCCGGCGTGAAA  20070
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8881   ATCAACAAGACCATGCCAAGCATCGAATCGCTGGTCAGTGACGGGCTGCCCGGCGTGAAA  8940

Query  20071  GCCGCCCTGACTCGAACAGCATCCAACATGAACGCGGCGGCGGACGTCTATGCGAAGACC  20130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8941   GCCGCCCTGACTCGAACAGCATCCAACATGAACGCGGCGGCGGACGTCTATGCGAAGACC  9000

Query  20131  GATCAGTCACTGGGAACCAGTTTGAGCCAGTATGCATTCGGCTCGTCGGGCGAAGGCCTG  20190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9001   GATCAGTCACTGGGAACCAGTTTGAGCCAGTATGCATTCGGCTCGTCGGGCGAAGGCCTG  9060
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Query  20191  GCTGGCGTCGCCTCGGTCGGTGGTCAGCCAAGTCAGGCTACCCAGCTGCTGAGCACACCC  20250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9061   GCTGGCGTCGCCTCGGTCGGTGGTCAGCCAAGTCAGGCTACCCAGCTGCTGAGCACACCC  9120

Query  20251  GTGTCACAGGTCACGACCCAGCTCGGCGAGACGGCCGCTGAGCTGGCACCCCGTGTTGTT  20310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9121   GTGTCACAGGTCACGACCCAGCTCGGCGAGACGGCCGCTGAGCTGGCACCCCGTGTTGTT  9180

Query  20311  GCGACGGTGCCGCAACTCGTTCAGCTGGCTCCGCACGCCGTTCAGATGTCGCAAAACGCA  20370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9181   GCGACGGTGCCGCAACTCGTTCAGCTGGCTCCGCACGCCGTTCAGATGTCGCAAAACGCA  9240

Query  20371  TCCCCCATCGCTCAGACGATCAGTCAAACCGCCCAACAGGCCGCCCAGAGCGCGCAGGGC  20430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9241   TCCCCCATCGCTCAGACGATCAGTCAAACCGCCCAACAGGCCGCCCAGAGCGCGCAGGGC  9300

Query  20431  GGCAGCGGCCCAATGCCCGCACAGCTTGCCAGCGCTGAAAAACCGGCCACCGAGCAAGCG  20490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9301   GGCAGCGGCCCAATGCCCGCACAGCTTGCCAGCGCTGAAAAACCGGCCACCGAGCAAGCG  9360

Query  20491  GAGCCGGTCCACGAAGTGACAAACGACGATCAGGGCGACCAGGGCGACGTGCAGCCGGCC  20550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9361   GAGCCGGTCCACGAAGTGACAAACGACGATCAGGGCGACCAGGGCGACGTGCAGCCGGCC  9420

Query  20551  GAGGTCGTTGCCGCGGCACGTGACGAAGGCGCCGGCGCATCACCGGGCCAGCAGCCCGGC  20610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9421   GAGGTCGTTGCCGCGGCACGTGACGAAGGCGCCGGCGCATCACCGGGCCAGCAGCCCGGC  9480

Query  20611  GGGGGCGTTCCCGCGCAAGCCATGGATACCGGAGCCGGTGCCCGCCCAGCGGCGAGTCCG  20670
               || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9481   GGAGGCGTTCCCGCGCAAGCCATGGATACCGGAGCCGGTGCCCGCCCAGCGGCGAGTCCG  9540

Query  20671  CTGGCGGCCCCCGTCGATCCGTCGACTCCGGCACCCTCAACAACCACAACGTTGTAGACC  20730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9541   CTGGCGGCCCCCGTCGATCCGTCGACTCCGGCACCCTCAACAACCACAACGTTGTAGACC  9600

Query  20731  GGGCCTGCCAGCGGCTCCGTCTCGCACGCAGCGCCTGTTGCTGTCCTGGCCTCGTCAGCA  20790
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  9601   GGGCCTGCCAGCGGCTCCGTCTCGCACGCAGCGCCTGTTGCTGTCCTGGCCTCGTCAGGA  9660

Query  20791  TGCGGCGGCCAGGGCCCGGTCGAGCAACCCGGTGACGTATTGCCAGTACAGCCAGTCCGC  20850
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9661   TGCGGCGGCCAGGGCCCGGTCGAGCAACCCGGTGACGTATTGCCAGTACAGCCAGTCCGC  9720

Query  20851  GACGGCCACACGCTGGACGGCCGCGTCAGTCGCAGTGTGCGCTTGGTGCAGGGCAATCTC  20910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9721   GACGGCCACACGCTGGACGGCCGCGTCAGTCGCAGTGTGCGCTTGGTGCAGGGCAATCTC  9780

Query  20911  CTGTGAGTGGGCAGCGTAGGCCCGGAACGCCCGCAGATGAGCGGCCTCGCGGCCGGTAGC  20970
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  9781   CTGTGAGTGGGCAGCGTAGGCCCGGAACGCCCGCAGATGAGCGGCCTCGCGGCCGGTAGC  9840

Query  20971  GGTGCTGGTCATGGGCTTCATCAGCTCGAACCACAGCATGTGCCGCTCATCGCCCGGTGG  21030
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9841   GGTGCTGGTCATGGGCTTCATCAGCTCGAACCACAGCATGTGCCGCTCATCGCCCGGTGG  9900

Query  21031  ATTGACATCCACCGGCGCCGGCGGCAACAAGTCGAGCAAACGCTGATCGGTAGTGTCGGC  21090
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9901   ATTGACATCCACCGGCGCCGGCGGCAACAAGTCGAGCAAACGCTGATCGGTAGTGTCGGC  9960

Query  21091  CAGCTGAGCCGCCGCCGAGGGGTCGACGACCTCCAGCCGCGACCGGCCCGTCATTTTGCC  21150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9961   CAGCTGAGCCGCCGCCGAGGGGTCGACGACCTCCAGCCGCGACCGGCCCGTCATTTTGCC  10020

Query  21151  GCTCTCCGGAATGTCATCTGGCTCCAGCACAATCTTGGCCACACCGGGATCCGAACTGGC  21210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10021  GCTCTCCGGAATGTCATCTGGCTCCAGCACAATCTTGGCCACACCGGGATCCGAACTGGC  10080

Query  21211  CAACTGCTCCGCGGTACCGATCACCGCCCGCAGCGTCATGTCGTGGAAAGCCGCCCAGGC  21270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10081  CAACTGCTCCGCGGTACCGATCACCGCCCGCAGCGTCATGTCGTGGAAAGCCGCCCAGGC  10140

Query  21271  TTGCACGGCCAAAACCGGGTAGGTGGCACAGCGTGCAATTTCGTCAACCGGGATTGCGTG  21330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10141  TTGCACGGCCAAAACCGGGTAGGTGGCACAGCGTGCAATTTCGTCAACCGGGATTGCGTG  10200

Query  21331  ATCCGCGCTGGCCAAGTACACCTTATTCGGCAATTCCATCCCGTCGGGTATGTAGGCCAG  21390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10201  ATCCGCGCTGGCCAAGTACACCTTATTCGGCAATTCCATCCCGTCGGGTATGTAGGCCAG  10260

Query  21391  CCCATAGCTGTTGGCCACGACGATGGAACCGTCGGTGGTCACCGCGGTGATCCAGAAGAA  21450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10261  CCCATAGCTGTTGGCCACGACGATGGAACCGTCGGTGGTCACCGCGGTGATCCAGAAGAA  10320

Query  21451  CCCGTAGTCGCCCGCGTTGTTGTCGGACGCGTTGAGCGCCGCCGCGATGCGTCGCGCCAA  21510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10321  CCCGTAGTCGCCCGCGTTGTTGTCGGACGCGTTGAGCGCCGCCGCGATGCGTCGCGCCAA  10380

Query  21511  CCGCAGCGCATCACCGCGGCCACGCTGGCGGGCGCTGGCAGCTGCAGTGGCGGCGTCGCG  21570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10381  CCGCAGCGCATCACCGCGGCCACGCTGGCGGGCGCTGGCAGCTGCAGTGGCGGCGTCGCG  10440

Query  21571  TGCCGCCCGAGCCGCCGACACCGGGATCATCGACACCGGCGTACCGTCATCTGCAGACTC  21630
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10441  TGCCGCCCGAGCCGCCGACACCGGGATCATCGACACCGGCGTACCGTCATCTGCAGACTC  10500

Query  21631  GCTGCGATCGGGTTTGTCGATGTGATCGGTCGACGGCGGGCGGGCAGGAGGTGCCGTCCG  21690
               |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  10501  GCTGCGATCGGGTTTGTCGATGTGATCGGTCGACGGAGGGCGGGCAGGAGGTGCCGTCCG  10560
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Query  21691  CGCCGAGGCCGCCCGCGTGCTCGGTGCCGCCGCCTTGTCCGAGGTAGCCACCGGCGCCCG  21750
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10561  CGCCGAGGCCGCCCGCGTGCTCGGTGCCGCCGCCTTGTCCGAGGTAGCCACCGGCGCCCG  10620

Query  21751  CCCAGTGGCAGCATGCGACCCCGCGCCCGAGGCCGCGGCCGTACCCACGCTCGAACGCGC  21810
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10621  CCCAGTGGCAGCATGCGACCCCGCGCCCGAGGCCGCGGCCGTACCCACGCTCGAACGCGC  10680

Query  21811  GCCCGCTCCCACGGCGGTACCG------CTCGGCGCGGCGGCCGCCGCCCGTGCGCCCGG  21864
               |||||||||||||||||||||      ||||||||||||||||||||||||||||||||
Sbjct  10681  GCCCGCTCCCACGGCGGTACCGGTACCGCTCGGCGCGGCGGCCGCCGCCCGTGCGCCCGG  10740

Query  21865  GACACCGGACGCCGCAGCCGGCGTCACCGACGCGGCGGATTCGTCCGCATGGGCAGGCCC  21924
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10741  GACACCGGACGCCGCAGCCGGCGTCACCGACGCGGCGGATTCGTCCGCATGGGCAGGCCC  10800

Query  21925  CGACTGCGTCCCCCCGCCCGCATGCTGGCCCGGCACACCAGGTTGCTCCGCCAACGCCGC  21984
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10801  CGACTGCGTCCCCCCGCCCGCATGCTGGCCCGGCACACCAGGTTGCTCCGCCAACGCCGC  10860

Query  21985  GGGTTTGACGTGCGGCGCCGGCTCGCCCCCTGGGGTGCCCGGTGTTGCTGGACCAGACGG  22044
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10861  GGGTTTGACGTGCGGCGCCGGCTCGCCCCCTGGGGTGCCCGGTGTTGCTGGACCAGACGG  10920

Query  22045  ACCGGGAGTGGCCGGTGTAACCGGCTGGGGCCCAGGCGATGGCGCCGGTGCCGGAGCCGG  22104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10921  ACCGGGAGTGGCCGGTGTAACCGGCTGGGGCCCAGGCGATGGCGCCGGTGCCGGAGCCGG  10980

Query  22105  CTGCGGGTGTGGAGCGGGAGCTGGGGTAACGGGCGTGGCCGGGGTTGCCGGTGTGGCCGG  22164
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10981  CTGCGGGTGTGGAGCGGGAGCTGGGGTAACGGGCGTGGCCGGGGTTGCCGGTGTGGCCGG  11040

Query  22165  GGCGACCGGGGGGGTGACCGGCGTGATCGGGGTTGGCTCGCCTGGTGTGCCCGGTTTGAC  22224
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11041  GGCGACCGGGGGGGTGACCGGCGTGATCGGGGTTGGCTCGCCTGGTGTGCCCGGTTTGAC  11100

Query  22225  CGGGGTCACCGGGGTGACCGGCTTGCCCGGGGTCACCGGCGTGACGGGAGTGCCGGGCGT  22284
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11101  CGGGGTCACCGGGGTGACCGGCTTGCCCGGGGTCACCGGCGTGACGGGAGTGCCGGGCGT  11160

Query  22285  TGGTGTGATCGGAGTTACCGGCGCTCCCGGGATGGGTGTGATTGGGGTTCCCGGGGTGA-  22343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  11161  TGGTGTGATCGGAGTTACCGGCGCTCCCGGGATGGGTGTGATTGGGGTTCCCGGGGTGAT  11220

Query  22344  -----------------TCGGGGTTCCCGGG-----------------GTGATCGGGGT  22368
                               |||||||||||||                 ||||||||||| 
Sbjct  11221  CGGGATTCCCGGCGTGATCGGGGTTCCCGGGGTGATCGGGGTTCCCGGCGTGATCGGGGT  11280

Query  22369  TCCCGGTGTGCCCGGTGTG---------CCCGGGGATGGCACGACCAGGGTAGGCACGTC  22419
               ||||||||||||||||||          |||||||||||||||||||||||||||||||| 
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Sbjct  11281  TCCCGGTGTGCCCGGTGTGCCCGGTGTGCCCGGGGATGGCACGACCAGGGTAGGCACGTC  11340

Query  22420  TGGGGGTGGCGGCGACTTCTGCTGAAGCAAATCCTCGAGTGCGTTCTTCGGAGGTTTCCA  22479
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11341  TGGGGGTGGCGGCGACTTCTGCTGAAGCAAATCCTCGAGTGCGTTCTTCGGAGGTTTCCA  11400

Query  22480  ATTCTTGGATTCCAGCACCCGCTCAGCGGTCTCGGCGACCAGACTGACATTGGCCCCATG  22539
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11401  ATTCTTGGATTCCAGCACCCGCTCAGCGGTCTCGGCGACCAGACTGACATTGGCCCCATG  11460

Query  22540  CGTCGCCGTGACCAATGAATTGATGGCGGTATGGCGCTCATCAGCATCCAGGCTAGGGTC  22599
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  11461  CGTCGCCGTGACCAATGAATTGATGGCGGTATGGCGCTCATCAGCATCCAGGCTAGAGTC  11520

Query  22600  ATTCTCCAGGATATCGATCTCCCGTTGAGCGCCATCCACATTATTGCCGATATCGGATTT  22659
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11521  ATTCTCCAGGATATCGATCTCCCGTTGAGCGCCATCCACATTATTGCCGATATCGGATTT  11580

Query  22660  AGCTTGCTCAATCAACCCGGCAATATGCCTGTGCCAGGTAATCACCGTGGCGAGATAATC  22719
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11581  AGCTTGCTCAATCAACCCGGCAATATGCCTGTGCCAGGTAATCACCGTGGCGAGATAATC  11640

Query  22720  CTGCAGCGTCATCAATTGATTGATGTTTGCACCCAGGGCGCCGTTGGCAGCATTGGCGGC  22779
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11641  CTGCAGCGTCATCAATTGATTGATGTTTGCACCCAGGGCGCCGTTGGCAGCATTGGCGGC  11700

Query  22780  GCCGCCGGACCATAGGCCGCCTTCGAAGACGTGGCCTTTCTGCTGGCGGCAGGTGTCCAA  22839
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11701  GCCGCCGGACCATAGGCCGCCTTCGAAGACGTGGCCTTTCTGCTGGCGGCAGGTGTCCAA  11760

Query  22840  TACATCGGTGACCCTTTGCAAAACCTGGCTATATTCCTGGGCCCGGTCATAGAAAGTGTC  22899
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11761  TACATCGGTGACCCTTTGCAAAACCTGGCTATATTCCTGGGCCCGGTCATAGAAAGTGTC  11820

Query  22900  TTCATCGGCTTCCACCCAGCCGCCCGGATCCAGCATCTGTCTGGCATAGCTGCCCGTCGG  22959
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11821  TTCATCGGCTTCCACCCAGCCGCCCGGATCCAGCATCTGTCTGGCATAGCTGCCCGTCGG  11880

Query  22960  CCTGGTAATACTCATCCCCTACTGCCCTCCCCAAACCGCCAGATCGCCTCGCGGATCACC  23019
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  23020  GTCCGGTTGGCCTCCGGCATTTCACGCCGGCTCGGCCGCTGGATCCACCCCGCGCCGGTA  23079
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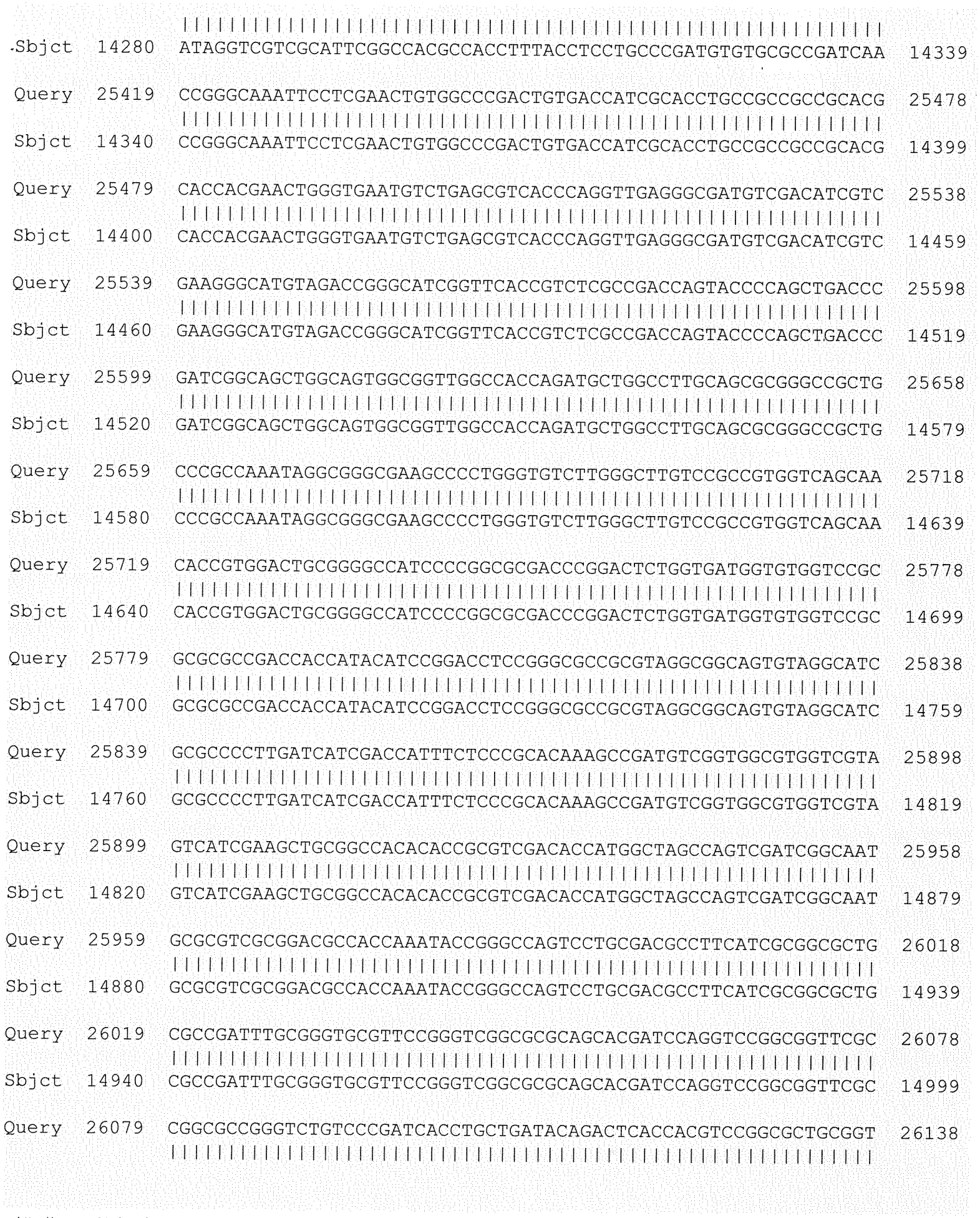
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16560  CCAGGTTCCGCCGGGACCCGTGGCGAAGCGTCGACACCGGTGTCGATCACCGCCACCGTC  16619

Query  27699  ACCCCGGCCCCGGTCGCGAACTTGTGGGCATCGGCCACGCCCAGATACGTGTTGCTCCAC  27758
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16620  ACCCCGGCCCCGGTCGCGAACTTGTGGGCATCGGCCACGCCCAGATACGTGTTGCTCCAC  16679

Query  27759  GGCGGATCGTGGAACCCGGACCCCGGCAGCGTGGTGGGCGACGCGCACAAAACGCGCTGT  27818
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16680  GGCGGATCGTGGAACCCGGACCCCGGCAGCGTGGTGGGCGACGCGCACAAAACGCGCTGT  16739

Query  27819  TCGGTAGGCTGATCCGGGCCCGTCACGTCGGGCGGCAACGCGCCCGGATCGATCGGCGGT  27878
               |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  16740  TCGGTAGGCTGATCCGGGCCCGCCACGTCGGGCGGCAACGCGCCCGGATCGATCGGCGGT  16799

Query  27879  GGCGTGATGGCCGATGCGGGCGACGCGGTGAGCAACGCCAGCGCCACCGTGATCAGAAAG  27938
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16800  GGCGTGATGGCCGATGCGGGCGACGCGGTGAGCAACGCCAGCGCCACCGTGATCAGAAAG  16859

Query  27939  ATACGGTGCACTCCCAGAACACTCCATTCGTTGAGATTCATTGCGATTCATTGAGCTGCG  27998
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16860  ATACGGTGCACTCCCAGAACACTCCATTCGTTGAGATTCATTGCGATTCATTGAGCTGCG  16919

Query  27999  TTGCTACCTTGGGCCACTTGACGGACCTGTGTGCATTTTAGACGTAACGGCTGGGCAAAC  28058
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16920  TTGCTACCTTGGGCCACTTGACGGACCTGTGTGCATTTTAGACGTAACGGCTGGGCAAAC  16979

Query  28059  AACGCTGTCACGCCTGGGCTGGTCCGCCGCGCCGACCAGGGCGCGTAGGCGCTGTACCTG  28118
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16980  AACGCTGTCACGCCTGGGCTGGTCCGCCGCGCCGACCAGGGCGCGTAGGCGCTGTACCTG  17039

Query  28119  GACCACGCCGGGACTCAACGGTTTTGCTACCGCACTAGCCGATATGCGGCTGCTACCAAA  28178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17040  GACCACGCCGGGACTCAACGGTTTTGCTACCGCACTAGCCGATATGCGGCTGCTACCAAA  17099

Query  28179  CGATCGCGGCCATGTCTCGGTTGTCTGAGCACACGCTGCGTATCGCGGCATCGATGTCGG  28238
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17100  CGATCGCGGCCATGTCTCGGTTGTCTGAGCACACGCTGCGTATCGCGGCATCGATGTCGG  17159

Query  28239  TGGCGGTGATGATCTGCAGATCCTGAACCGATACCGGTTGGCCCGCACGTTTTTGCGCAA  28298
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17160  TGGCGGTGATGATCTGCAGATCCTGAACCGATACCGGTTGGCCCGCACGTTTTTGCGCAA  17219

Query  28299  CCACCCGGGTGTCCCGGAACCCTTCGGCGCGTTCGATCACGTTGCGGGCGAACCGACCGT  28358
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17220  CCACCCGGGTGTCCCGGAACCCTTCGGCGCGTTCGATCACGTTGCGGGCGAACCGACCGT  17279
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Query  28359  TTTGCATAGCGTCGATACCGTGCTGCCCACTAGGGGTGGTGTAGTTACGGATGGTGGTGA  28418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17280  TTTGCATAGCGTCGATACCGTGCTGCCCACTAGGGGTGGTGTAGTTACGGATGGTGGTGA  17339

Query  28419  CCGCGTCGAGGAATACCTCCCGTGCGGCGTCATCGAGCTGGCTGGCGCGCGGTGTAGCGT  28478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17340  CCGCGTCGAGGAATACCTCCCGTGCGGCGTCATCGAGCTGGCTGGCGCGCGGTGTAGCGT  17399

Query  28479  AGCGGTGTCCAATCTCGACGATCTCCACCGGCGAATAAGACTCGAACCGCAGCTTTCGGT  28538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17400  AGCGGTGTCCAATCTCGACGATCTCCACCGGCGAATAAGACTCGAACCGCAGCTTTCGGT  17459

Query  28539  TGAACCGGCCAGCCAAACCCGGGTTCACGGTGAGGAATTC  28578
              ||||||||||||||||||||||||||||||||||||||||
Sbjct  17460  TGAACCGGCCAGCCAAACCCGGGTTCACGGTGAGGAATTC  17499
```

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.

Alignment B

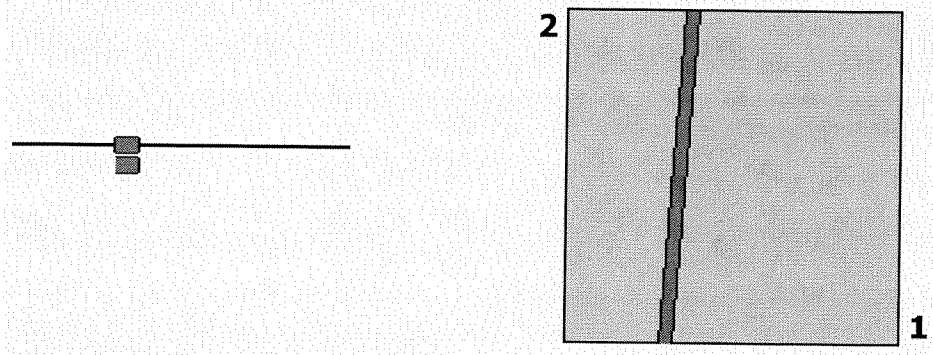
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 0 expect: 10.0 wordsize: 11 Filter ☐ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|40247167|emb|AX926815.1| Sequence 1 from Patent WO03085098
Length = 31808 (1 .. 31808)

Sequence 2: gi|40247218|emb|AX926827.1| Sequence 13 from Patent WO03085098
Length = 2244 (1 .. 2244)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 4315 bits (2244),  Expect = 0.0
 Identities = 2244/2244 (100%), Gaps = 0/2244 (0%)
 Strand=Plus/Plus

Query  9673   ATGACGACCAAGAAGTTCACTCCCACCATTACCCGTGGCCCCCGGTTGACCCCGGGCGAG  9732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      ATGACGACCAAGAAGTTCACTCCCACCATTACCCGTGGCCCCCGGTTGACCCCGGGCGAG  60

Query  9733   ATCAGCCTCACGCCGCCCGATGACCTGGGCATCGACATCCCACCGTCGGGCGTCCAAAAG  9792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     ATCAGCCTCACGCCGCCCGATGACCTGGGCATCGACATCCCACCGTCGGGCGTCCAAAAG  120
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Query  9793   ATCCTTCCCTACGTGATGGGTGGCGCCATGCTCGGCATGATCGCCATCATGGTGGCCGGC  9852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    ATCCTTCCCTACGTGATGGGTGGCGCCATGCTCGGCATGATCGCCATCATGGTGGCCGGC  180

Query  9853   GGCACCAGGCAGCTGTCGCCGTACATGTTGATGATGCCGCTGATGATGATCGTGATGATG  9912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    GGCACCAGGCAGCTGTCGCCGTACATGTTGATGATGCCGCTGATGATGATCGTGATGATG  240

Query  9913   GTCGGCGGTCTGGCCGGTAGCACCGGTGGTGGCGGCAAGAAGGTGCCCGAAATCAACGCC  9972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    GTCGGCGGTCTGGCCGGTAGCACCGGTGGTGGCGGCAAGAAGGTGCCCGAAATCAACGCC  300

Query  9973   GACCGCAAGGAGTACCTGCGGTATTTGGCAGGACTACGCACCCGAGTGACGTCCTCGGCC  10032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    GACCGCAAGGAGTACCTGCGGTATTTGGCAGGACTACGCACCCGAGTGACGTCCTCGGCC  360

Query  10033  ACCTCTCAGGTGGCGTTCTTCTCCTACCACGCACCGCATCCCGAGGATCTGTTGTCGATC  10092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    ACCTCTCAGGTGGCGTTCTTCTCCTACCACGCACCGCATCCCGAGGATCTGTTGTCGATC  420

Query  10093  GTCGGCACCCAACGGCAGTGGTCCCGGCCGGCCAACGCCGACTTCTATGCGGCCACCCGA  10152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421    GTCGGCACCCAACGGCAGTGGTCCCGGCCGGCCAACGCCGACTTCTATGCGGCCACCCGA  480

Query  10153  ATCGGTATCGGTGACCAGCCGGCGGTGGATCGATTATTGAAGCCGGCCGTCGGCGGGGAG  10212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481    ATCGGTATCGGTGACCAGCCGGCGGTGGATCGATTATTGAAGCCGGCCGTCGGCGGGGAG  540

Query  10213  TTGGCCGCCGCCAGCGCAGCACCTCAGCCGTTCCTGGAGCCGGTCAGTCATATGTGGGTG  10272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541    TTGGCCGCCGCCAGCGCAGCACCTCAGCCGTTCCTGGAGCCGGTCAGTCATATGTGGGTG  600

Query  10273  GTCAAGTTTCTACGAACCCATGGATTGATCCATGACTGCCCGAAACTGCTGCAACTCCGT  10332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601    GTCAAGTTTCTACGAACCCATGGATTGATCCATGACTGCCCGAAACTGCTGCAACTCCGT  660

Query  10333  ACCTTTCCGACTATCGCGATCGGCGGGGACTTGGCGGGGGCAGCCGGCCTGATGACGGCG  10392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661    ACCTTTCCGACTATCGCGATCGGCGGGGACTTGGCGGGGGCAGCCGGCCTGATGACGGCG  720

Query  10393  ATGATCTGTCACCTAGCCGTGTTCCACCCACCGGACCTGCTGCAGATCCGGGTGCTCACC  10452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721    ATGATCTGTCACCTAGCCGTGTTCCACCCACCGGACCTGCTGCAGATCCGGGTGCTCACC  780

Query  10453  GAGGAACCCGACGACCCCGACTGGTCCTGGCTCAAATGGCTTCCGCACGTACAGCACCAG  10512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781    GAGGAACCCGACGACCCCGACTGGTCCTGGCTCAAATGGCTTCCGCACGTACAGCACCAG  840

Query  10513  ACCGAAACCGATGCGGCCGGGTCCACCCGGCTGATCTTCACGCGCCAGGAAGGTCTGTCG  10572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  841    ACCGAAACCGATGCGGCCGGGTCCACCCGGCTGATCTTCACGCGCCAGGAAGGTCTGTCG  900

Query  10573  GACCTGGCCGCGCGCGGGCCACACGCACCCGATTCGCTTCCCGGCGGCCCCTACGTAGTC  10632
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901    GACCTGGCCGCGCGCGGGCCACACGCACCCGATTCGCTTCCCGGCGGCCCCTACGTAGTC  960

Query  10633  GTCGTCGACCTGACCGGCGGCAAGGCTGGATTCCCGCCCGACGGTAGGGCCGGTGTCACG  10692
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961    GTCGTCGACCTGACCGGCGGCAAGGCTGGATTCCCGCCCGACGGTAGGGCCGGTGTCACG  1020

Query  10693  GTGATCACGTTGGGCAACCATCGCGGCTCGGCCTACCGCATCAGGGTGCACGAGGATGGG  10752
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021   GTGATCACGTTGGGCAACCATCGCGGCTCGGCCTACCGCATCAGGGTGCACGAGGATGGG  1080

Query  10753  ACGGCTGATGACCGGCTCCCTAACCAATCGTTTCGCCAGGTGACATCGGTCACCGATCGG  10812
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081   ACGGCTGATGACCGGCTCCCTAACCAATCGTTTCGCCAGGTGACATCGGTCACCGATCGG  1140

Query  10813  ATGTCGCCGCAGCAAGCCAGCCGTATCGCGCGAAAGTTGGCCGGATGGTCCATCACGGGC  10872
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141   ATGTCGCCGCAGCAAGCCAGCCGTATCGCGCGAAAGTTGGCCGGATGGTCCATCACGGGC  1200

Query  10873  ACCATCCTCGACAAGACGTCGCGGGTCCAGAAGAAGGTGGCCACCGACTGGCACCAGCTG  10932
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201   ACCATCCTCGACAAGACGTCGCGGGTCCAGAAGAAGGTGGCCACCGACTGGCACCAGCTG  1260

Query  10933  GTCGGTGCGCAAAGTGTCGAGGAGATAACACCTTCCCGCTGGAGGATGTACACCGACACC  10992
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261   GTCGGTGCGCAAAGTGTCGAGGAGATAACACCTTCCCGCTGGAGGATGTACACCGACACC  1320

Query  10993  GACCGTGACCGGCTAAAGATCCCGTTTGGTCATGAACTAAAGACCGGCAACGTCATGTAC  11052
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321   GACCGTGACCGGCTAAAGATCCCGTTTGGTCATGAACTAAAGACCGGCAACGTCATGTAC  1380

Query  11053  CTGGACATCAAAGAGGGCGCGGAATTCGGCGCCGGACCGCACGGCATGCTCATCGGGACC  11112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381   CTGGACATCAAAGAGGGCGCGGAATTCGGCGCCGGACCGCACGGCATGCTCATCGGGACC  1440

Query  11113  ACGGGGTCTGGGAAGTCCGAATTCCTGCGCACCCTGATCCTGTCGCTGGTGGCAATGACT  11172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441   ACGGGGTCTGGGAAGTCCGAATTCCTGCGCACCCTGATCCTGTCGCTGGTGGCAATGACT  1500

Query  11173  CATCCAGATCAGGTGAATCTCCTGCTCACCGACTTCAAAGGTGGTTCAACCTTCCTGGGA  11232
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501   CATCCAGATCAGGTGAATCTCCTGCTCACCGACTTCAAAGGTGGTTCAACCTTCCTGGGA  1560

Query  11233  ATGGAAAAGCTTCCGCACACTGCCGCTGTCGTCACCAACATGGCCGAGGAAGCCGAGCTC  11292
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561   ATGGAAAAGCTTCCGCACACTGCCGCTGTCGTCACCAACATGGCCGAGGAAGCCGAGCTC  1620
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Query  11293  GTCAGCCGGATGGGCGAGGTGTTGACCGGAGAACTCGATCGGCGCCAGTCGATCCTCCGA  11352
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Sbjct  1621   GTCAGCCGGATGGGCGAGGTGTTGACCGGAGAACTCGATCGGCGCCAGTCGATCCTCCGA  1680

Query  11353  CAGGCCGGGATGAAAGTCGGCGCGGCCGGAGCCCTGTCCGGCGTGGCCGAATACGAGAAG  11412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681   CAGGCCGGGATGAAAGTCGGCGCGGCCGGAGCCCTGTCCGGCGTGGCCGAATACGAGAAG  1740

Query  11413  TACCGCGAACGCGGTGCCGACCTACCCCCGCTGCCAACGCTTTTCGTCGTCGTCGACGAG  11472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1741   TACCGCGAACGCGGTGCCGACCTACCCCCGCTGCCAACGCTTTTCGTCGTCGTCGACGAG  1800

Query  11473  TTCGCCGAGCTGTTGCAGAGTCACCCGGACTTCATCGGGCTGTTCGACCGGATCTGCCGC  11532
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1801   TTCGCCGAGCTGTTGCAGAGTCACCCGGACTTCATCGGGCTGTTCGACCGGATCTGCCGC  1860

Query  11533  GTCGGGCGGTCGCTGAGGGTCCATCTGCTGCTGGCTACCCAGTCGCTGCAGACCGGCGGT  11592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1861   GTCGGGCGGTCGCTGAGGGTCCATCTGCTGCTGGCTACCCAGTCGCTGCAGACCGGCGGT  1920

Query  11593  GTTCGCATCGACAAACTGGAGCCAAACCTGACATATCGAATCGCATTGCGCACCACCAGC  11652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1921   GTTCGCATCGACAAACTGGAGCCAAACCTGACATATCGAATCGCATTGCGCACCACCAGC  1980

Query  11653  TCTCATGAATCCAAGGCGGTAATCGGCACACCGGAGGCGCAGTACATCACCAACAAGGAG  11712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1981   TCTCATGAATCCAAGGCGGTAATCGGCACACCGGAGGCGCAGTACATCACCAACAAGGAG  2040

Query  11713  AGCGGTGTCGGGTTTCTCCGGGTCGGCATGGAAGACCCGGTCAAGTTCAGCACCTTCTAC  11772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2041   AGCGGTGTCGGGTTTCTCCGGGTCGGCATGGAAGACCCGGTCAAGTTCAGCACCTTCTAC  2100

Query  11773  ATCAGTGGGCCATACATGCCGCCGGCGGCAGGCGTCGAAACCAATGGTGAAGCCGGAGGG  11832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2101   ATCAGTGGGCCATACATGCCGCCGGCGGCAGGCGTCGAAACCAATGGTGAAGCCGGAGGG  2160

Query  11833  CCCGGTCAACAGACCACTAGACAAGCCGCGCGCATTCACAGGTTCACCGCGGCACCGGTT  11892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2161   CCCGGTCAACAGACCACTAGACAAGCCGCGCGCATTCACAGGTTCACCGCGGCACCGGTT  2220

Query  11893  CTCGAGGAGGCGCCGACACCGTGA  11916
              ||||||||||||||||||||||||
Sbjct  2221   CTCGAGGAGGCGCCGACACCGTGA  2244
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CPU time:      0.06 user secs.       0.03 sys. secs          0.09 total secs.
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Alignment C

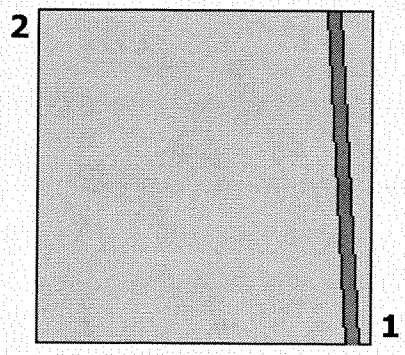
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 0 expect: 10.00 wordsize: 11 Filter ☐ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|40247167|emb|AX926815.1| Sequence 1 from Patent WO03085098
Length = 31808 (1 .. 31808)

Sequence 2: gi|40247268|emb|AX926841.1| Sequence 27 from Patent WO03085098
Length = 1857 (1 .. 1857)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

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 Score = 3571 bits (1857),  Expect = 0.0
 Identities = 1857/1857 (100%), Gaps = 0/1857 (0%)
 Strand=Plus/Minus

Query  28174  CCAAACGATCGCGGCCATGTCTCGGTTGTCTGAGCACACGCTGCGTATCGCGGCATCGAT  28233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1857   CCAAACGATCGCGGCCATGTCTCGGTTGTCTGAGCACACGCTGCGTATCGCGGCATCGAT  1798

Query  28234  GTCGGTGGCGGTGATGATCTGCAGATCCTGAACCGATACCGGTTGGCCCGCACGTTTTTG  28293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1797   GTCGGTGGCGGTGATGATCTGCAGATCCTGAACCGATACCGGTTGGCCCGCACGTTTTTG  1738
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Query  28294  CGCAACCACCCGGGTGTCCCGGAACCCTTCGGCGCGTTCGATCACGTTGCGGGCGAACCG  28353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1737   CGCAACCACCCGGGTGTCCCGGAACCCTTCGGCGCGTTCGATCACGTTGCGGGCGAACCG  1678

Query  28354  ACCGTTTTGCATAGCGTCGATACCGTGCTGCCCACTAGGGGTGGTGTAGTTACGGATGGT  28413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1677   ACCGTTTTGCATAGCGTCGATACCGTGCTGCCCACTAGGGGTGGTGTAGTTACGGATGGT  1618

Query  28414  GGTGACCGCGTCGAGGAATACCTCCCGTGCGGCGTCATCGAGCTGGCTGGCGCGCGGTGT  28473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1617   GGTGACCGCGTCGAGGAATACCTCCCGTGCGGCGTCATCGAGCTGGCTGGCGCGCGGTGT  1558

Query  28474  AGCGTAGCGGTGTCCAATCTCGACGATCTCCACCGGCGAATAAGACTCGAACCGCAGCTT  28533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1557   AGCGTAGCGGTGTCCAATCTCGACGATCTCCACCGGCGAATAAGACTCGAACCGCAGCTT  1498

Query  28534  TCGGTTGAACCGGCCAGCCAAACCCGGGTTCACGGTGAGGAATTCATCCACCTGATCCTC  28593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1497   TCGGTTGAACCGGCCAGCCAAACCCGGGTTCACGGTGAGGAATTCATCCACCTGATCCTC  1438

Query  28594  ATAGCCGGCCCCGATGAAACAGAAGTCGAATCGGTGTGTTTCCAATTGAACCAGGAGTTG  28653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1437   ATAGCCGGCCCCGATGAAACAGAAGTCGAATCGGTGTGTTTCCAATTGAACCAGGAGTTG  1378

Query  28654  ATTGACCGCCTCCATGCCGATCATGTCCGGTGTTCCGTCTTGATGACGTTCGATCAGCGA  28713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1377   ATTGACCGCCTCCATGCCGATCATGTCCGGTGTTCCGTCTTGATGACGTTCGATCAGCGA  1318

Query  28714  GTAGAACTCGTCCATGAAAATGATTCGCCCGAGTGACTTTTCGATCAGCTCGTTCGTCTT  28773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1317   GTAGAACTCGTCCATGAAAATGATTCGCCCGAGTGACTTTTCGATCAGCTCGTTCGTCTT  1258

Query  28774  GGGTCCTGACTCCCCGATGTAGTGCCCACAGAAGTCCGATCGGCGAACTTCTCGAATTTC  28833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1257   GGGTCCTGACTCCCCGATGTAGTGCCCACAGAAGTCCGATCGGCGAACTTCTCGAATTTC  1198

Query  28834  GGGGTGACGCACGATCCCCATGCCGGCGTAGATCTTGCCGAGCGCTTCAGCGGTGGTTGT  28893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1197   GGGGTGACGCACGATCCCCATGCCGGCGTAGATCTTGCCGAGCGCTTCAGCGGTGGTTGT  1138

Query  28894  CTTACCTGTGCCTGGTGGCCCCACCAGCAACATGTGGTTGGTCTGCCCCTCCACCGGTAG  28953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1137   CTTACCTGTGCCTGGTGGCCCCACCAGCAACATGTGGTTGGTCTGCCCCTCCACCGGTAG  1078

Query  28954  GCCGTGCTCTAGGCGCATCATGCGCACCTCGAGTTGGTCTTCCAGCGCCGATACCGCTTG  29013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1077   GCCGTGCTCTAGGCGCATCATGCGCACCTCGAGTTGGTCTTCCAGCGCCGATACCGCTTG  1018

Query  29014  CTTGACCGCCGCCAGGCCCACCTGTTTGGCCAGCAGTTCCCGGCCCTCGGCTAGCAGCTC  29073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1017   CTTGACCGCCGCCAGGCCCACCTGTTTGGCCAGCAGTTCCCGGCCCTCGGCTAGCAGCTC  958

Query  29074  GCCGCGCCGCTGCGCTGCATTGTCGTCATCGAGCTGGTCGCGGCTTTTCGCCGTCGAAGC  29133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  957    GCCGCGCCGCTGCGCTGCATTGTCGTCATCGAGCTGGTCGCGGCTTTTCGCCGTCGAAGC  898

Query  29134  ATCCCAACGGTCGGAGCGGCTGGCGATGGTTCGTTCATCGGTAACAATCAAGCGCAGGTT  29193
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  897    ATCCCAACGGTCGGAGCGGCTGGCGATGGTTCGTTCATCGGTAACAATCAAGCGCAGGTT  838

Query  29194  CGGGTCCGCCAGGGCTTCTTTGGCGGCGTCGGTGAGCACCCCGTTGATGGTGGCCTTCGA  29253
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  837    CGGGTCCGCCAGGGCTTCTTTGGCGGCGTCGGTGAGCACCCCGTTGATGGTGGCCTTCGA  778

Query  29254  CAGCCAGATCTGGGCCTTGTCCTCCTCATGCAGTTGCCGGTACACCATCCCCCGCACATA  29313
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  777    CAGCCAGATCTGGGCCTTGTCCTCCTCATGCAGTTGCCGGTACACCATCCCCCGCACATA  718

Query  29314  CGCCAAGTCGGCGACCAGCAGCGGAATATCGGCCGGTCCGATCGCCGCGGTGAGCACGTC  29373
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  717    CGCCAAGTCGGCGACCAGCAGCGGAATATCGGCCGGTCCGATCGCCGCGGTGAGCACGTC  658

Query  29374  GGCGCCGAACCGCTCCGATGACCTGCTGTGTCCGATCACGTCCACCCGGTCCAGCCAGTC  29433
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  657    GGCGCCGAACCGCTCCGATGACCTGCTGTGTCCGATCACGTCCACCCGGTCCAGCCAGTC  598

Query  29434  CAGGGCCACTCGCCCCTGCCCGAGATGGGCGGCGGCGTGGGCTGCCAGCGCACAAATCGA  29493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597    CAGGGCCACTCGCCCCTGCCCGAGATGGGCGGCGGCGTGGGCTGCCAGCGCACAAATCGA  538

Query  29494  CGCGGTCACCGCCGGCATGACGATCGCCTGTGGCGGCAGATCCTCGGCGGCCGTCGACAA  29553
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  537    CGCGGTCACCGCCGGCATGACGATCGCCTGTGGCGGCAGATCCTCGGCGGCCGTCGACAA  478

Query  29554  CACGTCGGGCCATCGCTGCGTGACGTACATCAGGAACGCCCGAGCCAGCTGATGCCACTG  29613
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477    CACGTCGGGCCATCGCTGCGTGACGTACATCAGGAACGCCCGAGCCAGCTGATGCCACTG  418

Query  29614  GTAGTTGCGCCACGAATCCAATAGCTCGCGGTTTGCTAACAGGGCATCGGCCTTCGCATA  29673
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  417    GTAGTTGCGCCACGAATCCAATAGCTCGCGGTTTGCTAACAGGGCATCGGCCTTCGCATA  358

Query  29674  CTCCCCCGCGATCGTCAACGCCGACGACAGCGCCAGCCCCACCTGAGATGCGTCGGTCAC  29733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  357    CTCCCCCGCGATCGTCAACGCCGACGACAGCGCCAGCCCCACCTGAGATGCGTCGGTCAC  298

Query  29734  CGTGATCCCGATGGATGGTCCCAGCTGGACCTCAGCGGCCAACGTCCGGCCGATCCGCGT  29793
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297    CGTGATCCCGATGGATGGTCCCAGCTGGACCTCAGCGGCCAACGTCCGGCCGATCCGCGT  238
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Query  29794  GGTCTCGCGGTGCAGCCACTCGCTATGGGCGTTGAGCTGCTTAAGCGAGGCCAGATCGCG  29853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237    GGTCTCGCGGTGCAGCCACTCGCTATGGGCGTTGAGCTGCTTAAGCGAGGCCAGATCGCG  178

Query  29854  GTCACCGCAGGCGATACGACCCAGCCACGCGTCGGCCATCGACGGATCGGCCTCGGTGGC  29913
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177    GTCACCGCAGGCGATACGACCCAGCCACGCGTCGGCCATCGACGGATCGGCCTCGGTGGC  118

Query  29914  AGCCACAAACTCAGGCAACGCCGCCACGCATCCCTGGCCATTCTTGATCGTCATCGCCCG  29973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  117    AGCCACAAACTCAGGCAACGCCGCCACGCATCCCTGGCCATTCTTGATCGTCATCGCCCG  58

Query  29974  ATCGAAATGCCGGCGCGCAGTGAGTAAATCACCCATCGTGTCCACCATTCTCGACAT  30030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  57     ATCGAAATGCCGGCGCGCAGTGAGTAAATCACCCATCGTGTCCACCATTCTCGACAT  1


CPU time:     0.05 user secs.      0.03 sys. secs      0.08 total secs.
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